



IFWO

RAW SEQUENCE LISTING

DATE: 10/07/2004

PATENT APPLICATION: US/10/820,712A

TIME: 09:40:10

Input Set : A:\251701.ST25.txt

Output Set: N:\CRF4\10072004\J820712A.raw

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3 <110> APPLICANT: KAO CORPORATION
4   Okuda, Mitsuyoshi
5   Izawa, Yoshifumi
6   Kobayashi, Tohru
7   Koyama, Shingo
8   Sato, Tsuyoshi
10 <120> TITLE OF INVENTION: ALKALINE PROTEASE
12 <130> FILE REFERENCE: 251701-US0
14 <140> CURRENT APPLICATION NUMBER: 10/820,712A
15 <141> CURRENT FILING DATE: 2004-04-09
17 <150> PRIOR APPLICATION NUMBER: 2003-106708
18 <151> PRIOR FILING DATE: 2003-04-10
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn version 3.2
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 434
26 <212> TYPE: PRT
27 <213> ORGANISM: Bacillus sp. KSM-KP43
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35 Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly
36          20          25          30
39 Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
40          35          40          45
43 Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
44          50          55          60
47 Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
48 65          70          75          80
51 Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser
52          85          90          95
55 Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln
56          100         105         110
59 Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn
60          115         120         125
63 Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn
64          130         135         140
67 Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala
68 145         150         155         160
71 Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala
72          165         170         175
75 Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe
76          180         185         190

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79 Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg
80      195      200      205
83 Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly
84      210      215      220
87 Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe
88 225      230      235      240
91 Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met
92      245      250      255
95 Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe
96      260      265      270
99 Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala
100      275      280      285
103 Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn
104      290      295      300
107 Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr
108 305      310      315      320
111 Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser
112      325      330      335
115 Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser
116      340      345      350
119 Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu
120      355      360      365
123 Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp
124      370      375      380
127 Phe Thr Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu
128 385      390      395      400
131 Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val
132      405      410      415
135 Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile
136      420      425      430
139 Val Asn
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144 <211> LENGTH: 1923
145 <212> TYPE: DNA
146 <213> ORGANISM: Bacillus sp. KSM-KP43
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150 <221> NAME/KEY: CDS
151 <222> LOCATION: (1)..(1920)
153 <220> FEATURE:
154 <221> NAME/KEY: sig_peptide
155 <222> LOCATION: (1)..(618)
157 <220> FEATURE:
158 <221> NAME/KEY: mat_peptide
159 <222> LOCATION: (619)..()
161 <400> SEQUENCE: 2
162 atg aga aag aag aaa aag gtg ttt tta tct gtt tta tca gct gca 45
163 Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala
164 -205 -200 -195
166 gcg att ttg tcg act gtt gcg tta agt aat cca tct gca ggt ggt 90

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167 Ala Ile  Leu Ser Thr Val Ala  Leu Ser Asn Pro Ser  Ala Gly Gly
168      -190      -185      -180
170 gca agg  aat ttt gat ctg gat  ttc aaa gga att cag  aca aca act      135
171 Ala Arg  Asn Phe Asp Leu Asp  Phe Lys Gly Ile Gln  Thr Thr Thr
172      -175      -170      -165
174 gat gct  aaa ggt ttc tcc aag  cag ggg cag act ggt  gct gct gct      180
175 Asp Ala  Lys Gly Phe Ser Lys  Gln Gly Gln Thr Gly  Ala Ala Ala
176      -160      -155      -150
178 ttt ctg  gtg gaa tct gaa aat  gtg aaa ctc cca aaa  ggt ttg cag      225
179 Phe Leu  Val Glu Ser Glu Asn  Val Lys Leu Pro Lys  Gly Leu Gln
180      -145      -140      -135
182 aag aag  ctt gaa aca gtc ccg  gca aat aat aaa ctc  cat att atc      270
183 Lys Lys  Leu Glu Thr Val Pro  Ala Asn Asn Lys Leu  His Ile Ile
184      -130      -125      -120
186 caa ttc  aat gga cca att tta  gaa gaa aca aaa cag  cag ctg gaa      315
187 Gln Phe  Asn Gly Pro Ile Leu  Glu Glu Thr Lys Gln  Gln Leu Glu
188      -115      -110      -105
190 aaa aca  ggg gca aag att ctc gac tac ata cct gat tat gct tac att      363
191 Lys Thr  Gly Ala Lys Ile Leu Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile
192      -100      -95      -90
194 gtc gag  tat gag ggc gat gtt aag tca gca aca agc acc att gag cac      411
195 Val Glu  Tyr Glu Gly Asp Val Lys Ser Ala Thr Ser Thr Ile Glu His
196      -85      -80      -75      -70
198 gtg gaa  tcc gtg gag cct tat ttg ccg ata tac aga ata gat ccc cag      459
199 Val Glu  Ser Val Glu Pro Tyr Leu Pro Ile Tyr Arg Ile Asp Pro Gln
200      -65      -60      -55
202 ctt ttc  aca aaa ggg gca tca gag ctt gta aaa gca gtg gcg ctt gat      507
203 Leu Phe  Thr Lys Gly Ala Ser Glu Leu Val Lys Ala Val Ala Leu Asp
204      -50      -45      -40
206 aca aag  cag aaa aat aaa gag gtg caa tta aga ggc atc gaa caa atc      555
207 Thr Lys  Gln Lys Asn Lys Glu Val Gln Leu Arg Gly Ile Glu Gln Ile
208      -35      -30      -25
210 gca caa  ttc gca ata agc aat gat gtg cta tat att acg gca aag cct      603
211 Ala Gln  Phe Ala Ile Ser Asn Asp Val Leu Tyr Ile Thr Ala Lys Pro
212      -20      -15      -10
214 gag tat  aag gtg atg aat gat gtt gcg cgt gga att gtc aaa gcg gat      651
215 Glu Tyr  Lys Val Met Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp
216      -5      -1  1      5      10
218 gtg gct  cag agc agc tac ggg ttg tat gga caa gga cag atc gta gcg      699
219 Val Ala  Gln Ser Ser Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala
220      15      20      25
222 gtt gcc  gat aca ggg ctt gat aca ggt cgc aat gac agt tcg atg cat      747
223 Val Ala  Asp Thr Gly Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His
224      30      35      40
226 gaa gcc  ttc cgc ggg aaa att act gca tta tat gca ttg gga cgg acg      795
227 Glu Ala  Phe Arg Gly Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr
228      45      50      55
230 aat aat  gcc aat gat acg aat ggt cat ggt acg cat gtg gct ggc tcc      843
231 Asn Asn  Ala Asn Asp Thr Asn Gly His Gly Thr His Val Ala Gly Ser

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232	60		65		70		75	
234	gta tta gga aac ggc tcc act aat aaa gga atg gcg cct cag gcg aat	891						
235	Val Leu Gly Asn Gly Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn							
236			80		85		90	
238	cta gtc ttc caa tct atc atg gat agc ggt ggg gga ctt gga gga cta	939						
239	Leu Val Phe Gln Ser Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu							
240			95		100		105	
242	cct tcg aat ctg caa acc tta ttc agc caa gca tac agt gct ggt gcc	987						
243	Pro Ser Asn Leu Gln Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala							
244			110		115		120	
246	aga att cat aca aac tcc tgg gga gca gca gtg aat ggg gct tac aca	1035						
247	Arg Ile His Thr Asn Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr							
248			125		130		135	
250	aca gat tcc aga aat gtg gat gac tat gtg cgc aaa aat gat atg acg	1083						
251	Thr Asp Ser Arg Asn Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr							
252	140		145		150		155	
254	atc ctt ttc gct gcc ggg aat gaa gga ccg aac ggc gga acc atc agt	1131						
255	Ile Leu Phe Ala Ala Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser							
256			160		165		170	
258	gca cca ggc aca gct aaa aat gca ata aca gtc gga gct acg gaa aac	1179						
259	Ala Pro Gly Thr Ala Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn							
260			175		180		185	
262	ctc cgc cca agc ttt ggg tct tat gcg gac aat atc aac cat gtg gca	1227						
263	Leu Arg Pro Ser Phe Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala							
264			190		195		200	
266	cag ttc tct tca cgt gga ccg aca aag gat gga ccg atc aaa ccg gat	1275						
267	Gln Phe Ser Ser Arg Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp							
268			205		210		215	
270	gtc atg gca ccg gga acg ttc ata cta tca gca aga tct tct ctt gca	1323						
271	Val Met Ala Pro Gly Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala							
272	220		225		230		235	
274	ccg gat tcc tcc ttc tgg gcg aac cat gac agt aaa tat gca tac atg	1371						
275	Pro Asp Ser Ser Phe Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met							
276			240		245		250	
278	ggt gga acg tcc atg gct aca ccg atc gtt gct gga aac gtg gca cag	1419						
279	Gly Gly Thr Ser Met Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln							
280			255		260		265	
282	ctt cgt gag cat ttt gtg aaa aac aga ggc atc aca cca aag cct tct	1467						
283	Leu Arg Glu His Phe Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser							
284			270		275		280	
286	cta tta aaa gcg gca ctg att gcc ggt gca gct gac atc ggc ctt ggc	1515						
287	Leu Leu Lys Ala Ala Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly							
288			285		290		295	
290	tac ccg aac ggt aac caa gga tgg gga cga gtg aca ttg gat aaa tcc	1563						
291	Tyr Pro Asn Gly Asn Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser							
292	300		305		310		315	
294	ctg aac gtt gcc tat gtg aac gag tcc agt tct cta tcc acc agc caa	1611						
295	Leu Asn Val Ala Tyr Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln							
296			320		325		330	

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298 aaa gcg acg tac tcg ttt act gct act gcc ggc aag cct ttg aaa atc      1659
299 Lys Ala Thr Tyr Ser Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile
300          335          340          345
302 tcc ctg gta tgg tct gat gcc cct gcg agc aca act gct tcc gta acg      1707
303 Ser Leu Val Trp Ser Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr
304          350          355          360
306 ctt gtc aat gat ctg gac ctt gtc att acc gct cca aat ggc aca cag      1755
307 Leu Val Asn Asp Leu Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln
308          365          370          375
310 tat gta gga aat gac ttt act tcg cca tac aat gat aac tgg gat ggc      1803
311 Tyr Val Gly Asn Asp Phe Thr Ser Pro Tyr Asn Asp Asn Trp Asp Gly
312 380          385          390          395
314 cgc aat aac gta gaa aat gta ttt att aat gca cca caa agc ggg acg      1851
315 Arg Asn Asn Val Glu Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr
316          400          405          410
318 tat aca att gag gta cag gct tat aac gta ccg gtt gga cca cag acc      1899
319 Tyr Thr Ile Glu Val Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr
320          415          420          425
322 ttc tcg ttg gca att gtg aat taa      1923
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324          430
327 <210> SEQ ID NO: 3
328 <211> LENGTH: 640
329 <212> TYPE: PRT
330 <213> ORGANISM: Bacillus sp. KSM-KP43
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338 Ala Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly
339 -190 -185 -180
342 Ala Arg Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr
343 -175 -170 -165
346 Asp Ala Lys Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala
347 -160 -155 -150
350 Phe Leu Val Glu Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln
351 -145 -140 -135
354 Lys Lys Leu Glu Thr Val Pro Ala Asn Asn Lys Leu His Ile Ile
355 -130 -125 -120
358 Gln Phe Asn Gly Pro Ile Leu Glu Glu Thr Lys Gln Gln Leu Glu
359 -115 -110 -105
362 Lys Thr Gly Ala Lys Ile Leu Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile
363 -100 -95 -90
366 Val Glu Tyr Glu Gly Asp Val Lys Ser Ala Thr Ser Thr Ile Glu His
367 -85 -80 -75 -70
370 Val Glu Ser Val Glu Pro Tyr Leu Pro Ile Tyr Arg Ile Asp Pro Gln
371 -65 -60 -55
374 Leu Phe Thr Lys Gly Ala Ser Glu Leu Val Lys Ala Val Ala Leu Asp
375 -50 -45 -40
378 Thr Lys Gln Lys Asn Lys Glu Val Gln Leu Arg Gly Ile Glu Gln Ile

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VERIFICATION SUMMARY

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